

SEQUENCE LISTING

<110> Nielsen, Bjarne R.  
Nielsen, Ruby  
Lehmbeck, Jan

<120> Thermostable Glucoamylase

<130> 5279.210-US

<160> 35

<170> PatentIn version 3.1

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<213> Talaromyces emersonii

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<221> misc\_feature  
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<223> Xaa at position 13 denotes an undetermined amino acid

<400> 1

Ala Asn Gly Ser Leu Asp Ser Phe Leu Ala Thr Glu Xaa Pro Ile Ala  
1 5 10 15

Leu Gln Gly Val Leu Asn Asn Ile Gly  
20 25

<210> 2  
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Val Gln Thr Ile Ser Asn Pro Ser Gly Asp Leu Ser Thr Gly Gly Leu  
1 5 10 15

Gly Glu Pro Lys  
20

<210> 3  
<211> 22  
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<213> Talaromyces emersonii

<220>  
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<222> (1)..(1)  
<223> Xaa in positions 1 denotes an undetermined amino acid

<220>  
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<222> (12)..(12)  
<223> Xaa in positions 12 denotes an undetermined amino acid

<400> 3

Xaa Asn Val Asn Glu Thr Ala Phe Thr Gly Pro Xaa Gly Arg Pro Gln  
1 5 10 15

Arg Asp Gly Pro Ala Leu  
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<210> 4  
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<400> 4

Asp Val Asn Ser Ile Leu Gly Ser Ile His Thr Phe Asp Pro Ala Gly  
1 5 10 15

Gly Cys Asp Asp Ser Thr Phe Gln Pro Cys Ser Ala Arg Ala Leu Ala  
20 25 30

Asn His Lys  
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Thr Xaa Ala Ala Ala Glu Gln Leu Tyr Asp Ala Ile Tyr Gln Trp Lys  
1 5 10 15

<210> 6

<211> 35  
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<400> 6

Ala Gln Thr Asp Gly Thr Ile Val Trp Glu Asp Asp Pro Asn Arg Ser  
1 5 10 15

Tyr Thr Val Pro Ala Tyr Cys Gly Gln Thr Thr Ala Ile Leu Asp Asp  
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Ser Trp Gln  
35

<210> 7  
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<400> 7

Ala Thr Gly Ser Leu Asp Ser Phe Leu Ala Thr Glu Thr Pro Ile Ala  
1 5 10 15

Leu Gln Gly Val Leu Asn Asn Ile Gly Pro Asn Gly Ala Asp Val Ala  
20 25 30

Gly Ala Ser Ala Gly Ile Val Val Ala Ser Pro Ser Arg Ser Asp Pro  
35 40 45

Asn Tyr Phe Tyr Ser Trp Thr Arg Asp Ala Ala Leu Thr Ala Lys Tyr  
50 55 60

Leu Val Asp Ala Phe Asn Arg Gly Asn Lys Asp Leu Glu Gln Thr Ile  
65 70 75 80

Gln Gln Tyr Ile Ser Ala Gln Ala Lys Val Gln Thr Ile Ser Asn Pro  
85 90 95

Ser Gly Asp Leu Ser Thr Gly Gly Leu Gly Glu Pro Lys Phe Asn Val  
100 105 110

Asn Glu Thr Ala Phe Thr Gly Pro Trp Gly Arg Pro Gln Arg Asp Gly  
115 120 125

Pro Ala Leu Arg Ala Thr Ala Leu Ile Ala Tyr Ala Asn Tyr Leu Ile  
130 135 140

Asp Asn Gly Glu Ala Ser Thr Ala Asp Glu Ile Ile Trp Pro Ile Val  
145 150 155 160

Gln Asn Asp Leu Ser Tyr Ile Thr Gln Tyr Trp Asn Ser Ser Thr Phe  
165 170 175

Asp Leu Trp Glu Glu Val Glu Gly Ser Ser Phe Phe Thr Thr Ala Val  
180 185 190

Gln His Arg Ala Leu Val Glu Gly Asn Ala Leu Ala Thr Arg Leu Asn  
195 200 205

His Thr Cys Ser Asn Cys Val Ser Gln Ala Pro Gln Val Leu Cys Phe  
210 215 220

Leu Gln Ser Tyr Trp Thr Gly Ser Tyr Val Leu Ala Asn Phe Gly Gly  
225 230 235 240

Ser Gly Arg Ser Gly Lys Asp Val Asn Ser Ile Leu Gly Ser Ile His  
245 250 255

Thr Phe Asp Pro Ala Gly Gly Cys Asp Asp Ser Thr Phe Gln Pro Cys  
260 265 270

Ser Ala Arg Ala Leu Ala Asn His Lys Val Val Thr Asp Ser Phe Arg  
275 280 285

Ser Ile Tyr Ala Ile Asn Ser Gly Ile Ala Glu Gly Ser Ala Val Ala  
290 295 300

Val Gly Arg Tyr Pro Glu Asp Val Tyr Gln Gly Gly Asn Pro Trp Tyr  
305 310 315 320

Leu Ala Thr Ala Ala Ala Glu Gln Leu Tyr Asp Ala Ile Tyr Gln  
325 330 335

Trp Lys Lys Ile Gly Ser Ile Ser Ile Thr Asp Val Ser Leu Pro Phe  
340 345 350

Phe Gln Asp Ile Tyr Pro Ser Ala Ala Val Gly Thr Tyr Asn Ser Gly

355

360

365

Ser Thr Thr Phe Asn Asp Ile Ile Ser Ala Val Gln Thr Tyr Gly Asp  
370 375 380

Gly Tyr Leu Ser Ile Val Glu Lys Tyr Thr Pro Ser Asp Gly Ser Leu  
385 390 395 400

Thr Glu Gln Phe Ser Arg Thr Asp Gly Thr Pro Leu Ser Ala Ser Ala  
405 410 415

Leu Thr Trp Ser Tyr Ala Ser Leu Leu Thr Ala Ser Ala Arg Arg Gln  
420 425 430

Ser Val Val Pro Ala Ser Trp Gly Glu Ser Ser Ala Ser Ser Val Leu  
435 440 445

Ala Val Cys Ser Ala Thr Ser Ala Thr Gly Pro Tyr Ser Thr Ala Thr  
450 455 460

Asn Thr Val Trp Pro Ser Ser Gly Ser Ser Thr Thr Thr Thr Ser  
465 470 475 480

Ser Ala Pro Cys Thr Thr Pro Thr Ser Val Ala Val Thr Phe Asp Glu  
485 490 495

Ile Val Ser Thr Ser Tyr Gly Glu Thr Ile Tyr Leu Ala Gly Ser Ile  
500 505 510

Pro Glu Leu Gly Asn Trp Ser Thr Ala Ser Ala Ile Pro Leu Arg Ala  
515 520 525

Asp Ala Tyr Thr Asn Ser Asn Pro Leu Trp Tyr Val Thr Val Asn Leu  
530 535 540

Pro Pro Gly Thr Ser Phe Glu Tyr Lys Phe Phe Lys Asn Gln Thr Asp  
545 550 555 560

Gly Thr Ile Val Trp Glu Asp Asp Pro Asn Arg Ser Tyr Thr Val Pro  
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ttg gca aat gtg att tcc aag cgc gcg acc ttg gat tca tgg ttg agc 96
Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
-5 -1 1 5

aac gaa gcg acc gtg gct cgt act gcc atc ctg aat aac atc ggg gcg 144
Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
10 15 20

gac ggt gct tgg gtg tcg ggc gcg gac tct ggc att gtc gtt gct agt 192
Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
25 30 35 40

ccc agc acg gat aac ccg gac tac ttc tac acc tgg act cgc gac tct 240
Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
45 50 55

ggc ctc gtc ctc aag acc ctc gtc gat ctc ttc cga aat gga gat acc 288
Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
60 65 70

agt ctc ctc tcc acc att gag aac tac atc tcc gcc cag gca att gtc 336
Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
75 80 85

cag ggt atc agt aac ccc tct ggt gat ctg tcc agc ggc gct ggt ctc 384
Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
90 95 100

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ggt gaa ccc aag ttc aat gtc gat gag act gcc tac act ggt tct tgg	432
Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp	
105 110 115 120	
gga cgg ccg cag cga gat ggt ccg gct ctg aga gca act gct atg atc	480
Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile	
125 130 135	
ggc ttc ggg cag tgg ctg ctt gac aat ggc tac acc agc acc gca acg	528
Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr	
140 145 150	
gac att gtt tgg ccc ctc gtt agg aac gac ctg tcg tat gtg gct caa	576
Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln	
155 160 165	
tac tgg aac cag aca gga tat gat ctc tgg gaa gaa gtc aat ggc tcg	624
Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser	
170 175 180	
tct ttc ttt acg att gct gtg caa cac cgc gcc ctt gtc gaa ggt agt	672
Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser	
185 190 195 200	
gcc ttc gcg acg gcc gtc ggc tcc tgc tcc tgg tgt gat tct cag	720
Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln	
205 210 215	
gca ccc gaa att ctc tgc tac ctg cag tcc ttc tgg acc ggc agc ttc	768
Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe	
220 225 230	
att ctg gcc aac ttc gat agc agc cgt tcc ggc aag gac gca aac acc	816
Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr	
235 240 245	
ctc ctg gga agc atc cac acc ttt gat cct gag gcc gca tgc gac gac	864
Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp	
250 255 260	
tcc acc ttc cag ccc tgc tcc ccg cgc gcg ctc gcc aac cac aag gag	912
Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu	
265 270 275 280	
gtt gta gac tct ttc cgc tca atc tat acc ctc aac gat ggt ctc agt	960
Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser	
285 290 295	
gac agc gag gct gtt gcg gtg ggt cgg tac cct gag gac acg tac tac	1008
Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr	
300 305 310	
aac ggc aac ccg tgg ttc ctg tgc acc ttg gct gcc gca gag cag ttg	1056
Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Glu Gln Leu	
315 320 325	

tac gat gct cta tac cag tgg gac aag cag ggg tcg ttg gag gtc aca Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr 330 335 340	1104
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gtg aag act ttc gcc gat ggc ttc gtc tct att gtg gaa act cac gcc Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala 380 385 390	1248
gca agc aac ggc tcc atg tcc gag caa tac gac aag tct gat ggc gag Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu 395 400 405	1296
cag ctt tcc gct cgc gac ctg acc tgg tct tat gct gct ctg ctg acc Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr 410 415 420	1344
gcc aac aac cgt cgt aac tcc gtc gtg cct gct tct tgg ggc gag acc Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr 425 430 435 440	1392
tct gcc agc agc gtg ccc ggc acc tgt gcg gcc aca tct gcc att ggt Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly 445 450 455	1440
acc tac agc agt gtg act gtc acc tcg tgg ccg agt atc gtg gct act Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr 460 465 470	1488
ggc ggc acc act acg acg gct acc ccc act gga tcc ggc agc gtg acc Gly Gly Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr 475 480 485	1536
tcg acc agc aag acc acc gcg act gct agc aag acc agc acc acg acc Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Thr Thr 490 495 500	1584
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 <212> PRT  
 <213> Aspergillus niger

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Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly

-20

-15

-10

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-5 -1 1 5

Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala  
10 15 20

Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser  
25 30 35 40

Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser  
45 50 55

Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr  
60 65 70

Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val  
75 80 85

Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu  
90 95 100

Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp  
105 110 115 120

Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile  
125 130 135

Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr  
140 145 150

Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln  
155 160 165

Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser  
170 175 180

Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser  
185 190 195 200

Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln  
205 210 215

Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe  
220 225 230

Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr  
235 240 245

Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp  
250 255 260

Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu  
265 270 275 280

Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser  
285 290 295

Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr  
300 305 310

Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu  
315 320 325

Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr  
330 335 340

Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr  
345 350 355 360

Gly Thr Tyr Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala  
365 370 375

Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala  
380 385 390

Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu  
395 400 405

Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr  
410 415 420

Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr  
425 430 435 440

Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly  
445 450 455

Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr  
460 465 470

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Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Thr Thr  
490 495 500

Arg Ser Gly Met Ser Leu  
505 510

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Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala  
35 40 45

Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser  
50 55 60

Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser  
65 70 75 80

Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr  
85 90 95

Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val  
100 105 110

Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu  
115 120 125

Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp  
130 135 140

Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile  
145 150 155 160

Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr  
165 170 175

Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln  
180 185 190

Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser  
195 200 205

Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser  
210 215 220

Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln  
225 230 235 240

Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe  
245 250 255

Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr  
260 265 270

Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp  
275 280 285

Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu  
290 295 300

Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser  
305 310 315 320

Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr  
325 330 335

Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu  
340 345 350

Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr  
355 360 365

Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr  
370 375 380

Gly Thr Tyr Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala  
385 390 395 400

Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala  
405 410 415

Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu  
420 425 430

Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr  
435 440 445

Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr  
450 455 460

Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly  
465 470 475 480

Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr  
485 490 495

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500 505 510

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Arg Ser Gly Met Ser Leu  
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<223> n in position 3 = A, G, C, T
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17

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<223> n= A, G, C, T
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<220>
<221> misc_feature
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<223> n= A, G, C, T
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17

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17

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17

<210> 15  
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<220>  
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<400> 16  
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21

<210> 18

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<210> 21
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tagatcaaga cgagtactct gattgagctg caggcttggaa atatatgatt agcagaaaaaa	180	
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Val Glu Gly Ser Ser Phe Phe Thr Thr Ala Val Gln His Arg Ala Leu  
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